

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2001, 16:26:03 ; Search time 29.37 Seconds
(without alignments)
23.091 Million cell updates/sec

Title: US-09-331-631A-38
Perfect score: 53
Sequence: 1 CXXXXXXXXXXXXXXCXXC 21

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	37	1	TXP3_APTSC
2	53	100.0	39	1	CYGN_CYGAT
3	53	100.0	40	1	MED6_MELGA
4	53	100.0	45	1	M84C_DROME
5	53	100.0	56	1	AMCI_APIME
6	53	100.0	57	1	MT2_SCYSE
7	53	100.0	58	1	MT1_HOMAM
8	53	100.0	58	1	MT1_SCYSE
9	53	100.0	58	1	MT2_CALSI
10	53	100.0	58	1	MT_ASTFL
11	53	100.0	58	1	MT_CARMA
12	53	100.0	59	1	MT_PORPO
13	53	100.0	59	1	MT1_CALSI
14	53	100.0	62	1	MT1_CANGA
15	53	100.0	63	1	M84A_DROME
16	53	100.0	68	1	M84D_DROME
17	53	100.0	70	1	SIX1_LEIOU
18	53	100.0	72	1	MT11_MYTED
19	53	100.0	72	1	MT12_MYTED
20	53	100.0	72	1	MT13_MYTED
21	53	100.0	72	1	MT14_MYTED
22	53	100.0	74	1	M84B_DROME
23	53	100.0	83	1	MEX1_DROME
24	53	100.0	88	1	SIX1_ANDAU
25	53	100.0	88	1	SIX1_MESMA
26	53	100.0	88	1	SIX2_ANDAU
27	53	100.0	94	1	SIXE_BUTJU
28	53	100.0	95	1	KRF4_ANAPL
29	53	100.0	95	1	KRF4_COLLI
30	53	100.0	97	1	KRF4_COLLI
31	53	100.0	97	1	KRFB_CHICK
32	53	100.0	97	1	KRFB_CHICK
33	53	100.0	97	1	KRFD_CHICK

34	53	100.0	98	1	KRFT_LARNO	P02451	larus novae
35	53	100.0	105	1	YG44_YEAST	P53299	saccharomyc
36	53	100.0	107	1	INB3_CAEL	O09628	caenorhabdi
37	53	100.0	107	1	TAP1_ANTMA	O04189	antirrhinum
38	53	100.0	115	1	A62E_DROME	O46202	drosophilla
39	53	100.0	157	1	VE5_RHRYL	P24834	rhesus papl
40	53	100.0	178	1	CHHC_BOMO	P20730	bombyx mori
41	53	100.0	194	1	KRUB_HUMAN	O75690	homo sapien
42	53	100.0	369	1	PP11_HUMAN	P21128	homo sapien
43	53	100.0	399	1	IG1R_MOUSE	O60751	mus musculus
44	53	100.0	459	1	VTNC_PTG	P48819	sus scrofa
45	53	100.0	467	1	D4DR_HUMAN	P21917	homo sapien

ALIGNMENTS

```
RESULT 1
ID TXP3_APTSC STANDARD; PRT; 37 AA.
AC P49268;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE APTOTOXIN III (PARALYTIC PEPTIDE III) (PP III).
OS Aptostichus schlingeri (Trap-door spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Mygalomorphae; Cyrtachenidae; Aptostichus.
RN [1]
RP SEQUENCE:
RC TISSUE=VENOM;
RX MEDLINE=93069259; PubMed=1440641;
RA Skinner W.S., Dennis P.A., Li J.P., Quistad G.B.;
RT "Identification of insecticidal peptides from venom of the trap-door
RT spider, Aptostichus schlingeri (Ctenizidae).";
RL Toxicon 30:1043-1050(1992).
RC -1- FUNCTION: IS BOTH PARALYTIC AND LETHAL, WHEN INJECTED INTO
CC LEPIDOPTERAN LARVAE. IS A SLOWER ACTING TOXIN, BEING LETHAL AT 24
CC HR, BUT NOT PARALYTIC AT 1 HR POST-INJECTION.
CC -1- PTM: FOUR DISULFIDE BONDS ARE PRESENT.
CC -1- MISCELLANEOUS: LD50 IS 0.50 MG/KG BY SUBCUTANEOUS INJECTION.
CC -1- SIMILARITY: TO APTOTOXIN VII.
KW Venom; Toxin.
SQ SEQUENCE 37 AA; 3769 MW; C8D01091694E1908 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 37;
Best local Similarity 19.0%; Pred. No. 40;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXCXXC 21
DB 15 CGGKCAVWNCIGGCKSTC 35

RESULT 2
ID CYGN_CYGAT STANDARD; PRT; 39 AA.
AC P02785;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE CYGNIN.
OS Cygnus atratus (Black swan).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Cygnus.
RN [1]
RP SEQUENCE:
RC TISSUE=EGG WHITE;
RX MEDLINE=84087048; PubMed=6654595;
RA Simpson R.J., Morgan F.J.;
RT "Isolation and complete amino acid sequence of a basic low molecular
RT weight protein from black swan egg white.";
```

```

RL Int. J. Pept. Protein Res. 22:476-481(1983).
CC -I- FUNCTION: NOT KNOWN.
CC -I- SIMILARITY: STRONG, TO TURKEY MELEAGRIN, AND SOME, TO A PART
CC (EXON 9) OF TRANSFERRINS.
DR PIR: A03258; IZMS.
KW Egg white.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 6 33 OR 6-32 (BY SIMILARITY).
FT DISULFID 12 28 BY SIMILARITY.
FT DISULFID 16 32 OR 16-33 (BY SIMILARITY).
SQ SEQUENCE 39 AA: 4452 MW: 805DE270495FB4AA CRC64;

Query Match 100.0%; Score 53; DB 1; Length 39;
Best Local Similarity 19.0%; Pred. No. 42;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXXXXXXXXXXXXXXX 21
DB 12 CSSKCSKADVWVLSDDCKFC 32

RESULT 3
MEIG.MEIGA STANDARD: PRT; 40 AA.
AC P21376;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE MELEAGRIN.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=89340398; PubMed=2760022;
RA Odani S., Koide T., Ono T., Takahashi Y., Suzuki J.-I.;
RT "Covalent structure of a low-molecular-mass protein, meleagrin,
RT present in a turkey (Meleagris gallopavo) ovomucoid preparation.";
RC J. Biochem. 105:660-663(1989).
CC -I- FUNCTION: NOT KNOWN.
CC -I- SIMILARITY: STRONG, TO BLACK SWAN CYGNIN, AND SOME, TO A PART
CC (EXON 9) OF TRANSFERRINS.
DR PIR: JX0070; JX0070.
KW Egg white.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 6 33 OR 6-32.
FT DISULFID 12 28
FT DISULFID 16 32 OR 16-33.
SQ SEQUENCE 40 AA: 4552 MW: 2B6C78FE5B302AA4 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 40;
Best Local Similarity 19.0%; Pred. No. 42;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXXXXXXXXXXXXXXX 21
DB 12 CSSKCSKAEMVWVSPDCKVHC 32

RESULT 4
M84C.DROME STANDARD: PRT; 55 AA.
AC Q01644; OSVIAO;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE MALE SPECIFIC SPERM PROTEIN M84DC.
GN M84DC.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

```

```

OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RX MEDLINE=92102953; PubMed=1684716;
RA Kuhn R., Kuhn C., Boersch D., Glaetzer K.H., Schaefer U.,
RA Schaefer M.;
RT "A cluster of four genes selectively expressed in the male germ line
RT of Drosophila melanogaster";
RL Mech. Dev. 35:143-151(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Balwin D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Suton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferlita S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -I- TISSUE SPECIFICITY: TESTIS.
CC -I- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCYTES.
CC -I- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPEITIVE C-G-P
CC MOTIFS.
CC -I- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X67703; CAA47939.1; -
CC EMBL: AE003672; AAF54025.1; -
CC DR HSSP: P01180; INPO.
CC FLYBASE: FBgn0004174; M84DC.
CC Spermatoogenesis; Repeat; Multigene family.
KW SEQUENCE 55 AA: 5225 MW: 95A12F3AEC8B06C CRC64;

```

```

Query Match          100.0%: Score 53; DB 1; Length 55;
Best Local Similarity 19.0%: Pred. No. 52;
Matches      4; Conservative 17; Mismatches      0; Indels      0; Gaps      0;

QY      1 CXXXCXXXXXXXXXXXXCXXC 21
        1::1:::|||||:|||||
DB      2 CCGPCGSCGGYCGCGPC 22

RESULT 5
AMCI_APIME STANDARD: PRT; 56 AA.
AC P56682:
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CHYMOTRYPSIN INHIBITOR (AMCI).
OS Apis mellifera (honeybee).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Apis.
RN (1)
RP SEQUENCE, AND STRUCTURE BY NMR.
RC TISSUE=HEMOLYMPH;
RX MEDLINE=99339335; PubMed=10411628;
RA Bania J., Stachowiak D., Polanowski A.;
RT "Primary structure and properties of the cathepsin G/chymotrypsin
RT inhibitor from the larval hemolymph of Apis mellifera.";
RL Eur. J. Biochem. 262:680-687(1999).
CC -1- FUNCTION: CHYMOTRYPSIN AND CATHEPSIN G INHIBITOR.
CC -1- SUBCELLULAR LOCATION: SECRETED.
DR PDB: 1CCY; 12-MAR-99.
DR INTERPRO: IPR002919; -.
DR PRAM: PF01826; T1L; 1.
RW Serine protease inhibitor; 3D-structure.
FT FT DISULFID 3 36
FT FT DISULFID 12 32
FT FT DISULFID 16 28
FT FT DISULFID 20 56
FT FT DISULFID 38 50
FT FT DISULFID 56 AA; 5973 MW; 092B2815AE6B2B7F CRC64;
SO

Query Match          100.0%: Score 53; DB 1; Length 56;
Best Local Similarity 19.0%: Pred. No. 53;
Matches      4; Conservative 17; Mismatches      0; Indels      0; Gaps      0;

QY      1 CXXXCXXXXXXXXXXXXCXXC 21
        1::1:::|||||:|||||
DB      12 CGSACAPTCAGPKRTICMGC 32

RESULT 6
MT2_SCYSE STANDARD: PRT; 57 AA.
AC P02806:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-II (MT-II).
OS Scyllia serrata (Mud crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Scyllia.
RN (1)
RP SEQUENCE.
RX MEDLINE=82142340; PubMed=7061431;
RA Lerch K., Ammer D., Olafson R.W.;
RT "Crab metallothionein. Primary structures of metallothioneins 1 and
RT 2.";
J. Biol. Chem. 257:2420-2426(1982).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE

```

CC	RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN MARINE
CC	CYSTINE ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS
CC	OF HEAVY-METAL IONS.
CC	-I- SMIITARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY
DR	PIR; A03284; SMK025.
DR	HSSP; P35949; IDMF.
DR	INTERPRO; IPRO02045; -.
DR	INTERPRO; IPRO03019; -.
DR	Pfam; PF00131; metalthio; 1.
DR	PRINTS; PRO0858; MCR0STCEAN.
KW	Metal-binding: Metal-thiolate cluster; Chelation.
FT	DOMAIN 1 28 BETA.
FT	DOMAIN 29 57 ALPHA.
FT	METAL 4 4 CLUSTER B.
FT	METAL 5 5 CLUSTER B.
FT	METAL 9 9 CLUSTER B.
FT	METAL 11 11 CLUSTER B.
FT	METAL 16 16 CLUSTER B.
FT	METAL 20 20 CLUSTER B.
FT	METAL 22 22 CLUSTER B.
FT	METAL 25 25 CLUSTER B.
FT	METAL 27 27 CLUSTER B.
FT	METAL 30 30 CLUSTER A.
FT	METAL 33 33 CLUSTER A.
FT	METAL 37 37 CLUSTER A.
FT	METAL 39 39 CLUSTER A.
FT	METAL 45 45 CLUSTER A.
FT	METAL 49 49 CLUSTER A.
FT	METAL 53 53 CLUSTER A.
FT	METAL 55 55 CLUSTER A.
FT	METAL 56 56 CLUSTER A.
SQ	SEQUENCE 57 AA; 6109 MW; 8C2B3f6A6BAA3611 CRC64;

```

Query Match          100.0%; Score 53; DB 1; Length 57;
Best Local Similarity 19.0%; Pred. No. 53;
Matches          4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY      1 CXXXCXXXXXXXXXXXXXCC 21
          |::|:::|:::|:::|
DB      33 CSSGCKANKEDCRKTCSKPC 53

RESULT  7
ID      MT1_HOMAM          STANDARD;          PRT;          58 AA.
AC      P29499;
DT      01-APR-1993 (Rel. 25, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      01-NOV-1997 (Rel. 35, Last annotation update)
DE      METALLOTHIONEIN-1 (CUMT-1).
OS      Homarus americanus (American lobster).
OC      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC      Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC      Nephropoidea; Nephropidae; Homarus.
RN      [1]
RP      SEQUENCE.
RC      TISSUE=HEPATOPANCREAS;
RX      MEDLINE=89215793; PubMed=2709004;
RA      Brouwer M., Winge D.R., Gray W.R.;
RT      "Structural and functional diversity of copper-metallothioneins from
RL      the American lobster Homarus americanus.";
RN      J. Inorg. Biochem. 35:289-303(1989).
RN      [2]
RP      STRUCTURE BY NMR.
RX      MEDLINE=94318629; PubMed=8043573;
RA      Zhu Z., Derosé E.F., Mullen G.P., Petering D.H., Shaw C.F. III;
RT      "Sequential proton resonance assignments and metal cluster topology
RL      of lobster metallothionein-1.";
RN      Biochemistry 33:8858-8865(1994).
CC      -I- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC      RESIDUES THAT BIND VARIOUS HEAVY METALS. THE DIFFERENT FORMS OF
CC      LOBSTER METALLOTHIONEINS MAY HAVE DIFFERENT BIOLOGICAL FUNCTIONS.

```


FT METAL 34 34 CLUSTER A.
FT METAL 38 38 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 46 46 CLUSTER A.
FT METAL 50 50 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 56 56 CLUSTER A.
FT METAL 57 57 CLUSTER A.
FT VARIANT 1 1 MISSING (IN MT-11A).
SQ SEQUENCE 58 AA; 6287 MM; EF679CB94975C5F0 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 58;
Best Local Similarity 19.0%; Pred. No. 54;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXX 21
DB 34 CSSECKCTSKESCKTCKPC 54

RESULT 10
MT_ASTFL STANDARD; PRT; 58 AA.
ID MT_ASTFL
AC P55951;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN (MT).
OS Astacus fluviatilis (Broad-fingered crayfish) (Astacus astacus).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidae; Astacidae; Astacus.
RN [1]
RP SEQUENCE.
RC TISSUE-MIDGUT;
RX MEDLINE-97079279; PubMed-8921011;
RA Pedersen S.N., Pedersen K.L., Hoejrup P., Depledge M.H., Knudsen J.;
RT Primary structures of decapod crustacean metallothioneins with special emphasis on freshwater and semi-terrestrial species.";
RL Biochem. J. 319:999-1003(1996).

CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN CRUSTACEA
ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS OF HEAVY-
METAL IONS.
CC -1- INDUCTION: BY CADMIUM.
CC -1- MASS SPECTROMETRY: MN-5910.8; METHOD-MALDI.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR HSSP; P55949; IDMD.
DR INTERPRO; IPR002045; -;
DR PRAM; PF00131; metalthio; 1.
DR PRINTS; PR00856; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.
FT DOMAIN 1 29 ALPHA.
FT METAL 30 58 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 10 10 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 17 17 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 26 26 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 31 31 CLUSTER A.
FT METAL 34 34 CLUSTER A.
FT METAL 38 38 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 46 46 CLUSTER A.
FT METAL 50 50 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 56 56 CLUSTER A.

FT METAL 57 57 CLUSTER A.
FT VARIANT 1 1 MISSING (IN VARIANT ISOLATED IN LOW
CADMIUM CONCENTRATION).
SQ SEQUENCE 58 AA; 5911 MM; 576365B3EE5C7122 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 58;
Best Local Similarity 19.0%; Pred. No. 54;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXX 21
DB 34 CTGCKPCPSKECAKCTCKPC 54

RESULT 11
MT_CARMA STANDARD; PRT; 58 AA.
ID MT_CARMA
AC P55948;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE METALLOTHIONEIN (MT).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
RN [1]
RP SEQUENCE.
RC TISSUE-MIDGUT;
RX MEDLINE-94153337; PubMed-8110201;
RA Pedersen K.L., Pedersen S.N., Hoejrup P., Andersen J.S.,
RA Roepstorff P., Knudsen J., Depledge M.H.;
RT Purification and characterization of a cadmium-induced metallothionein from the shore crab Carcinus maenas (L.).";
RL Biochem. J. 297:609-614(1994).

CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN MARINE
CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS
OF HEAVY-METAL IONS.
CC -1- INDUCTION: BY CADMIUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR HSSP; P55949; IDMD.
DR INTERPRO; IPR002045; -;
DR PRAM; PF00131; metalthio; 1.
DR PRINTS; PR00856; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.
FT DOMAIN 1 29 ALPHA.
FT METAL 30 58 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 10 10 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 17 17 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 26 26 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 31 31 CLUSTER A.
FT METAL 34 34 CLUSTER A.
FT METAL 38 38 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 46 46 CLUSTER A.
FT METAL 50 50 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 56 56 CLUSTER A.
FT METAL 57 57 CLUSTER A.
FT VARIANT 1 1 MISSING (IN VARIANT ISOLATED IN LOW
CADMIUM CONCENTRATION).
SQ SEQUENCE 58 AA; 6133 MM; 0167CDA2E9C9731D CRC64;


```

RESULT 14
MT1-CANGA STANDARD; PRT; 62 AA.
ID MT1-CANGA
AC P51113
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-1.
GN MT-1.
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC anamorphic Saccharomycetales; Candida.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90062075; Pubmed=2584191;
RA Mehra R.K., Garey J.R., Butt T.R., Gray W.R., Winge D.R.;
RT "Candida glabrata metallothioneins. Cloning and sequence of the genes
RT and characterization of proteins.";
RL J. Biol. Chem. 264:19747-19753(1989).
RN [2]
RP SEQUENCE OF 1-16.
RX MEDLINE=89057829; Pubmed=3194392;
RA Mehra R.K., Tarbet B.E., Gray W.R., Winge D.R.;
RT "Metal-specific synthesis of two metallothioneins and gamma-glutamyl
RT peptides in Candida glabrata.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:8815-8819(1988).
CC -1- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
CC SEQUESTRATION OF TOXIC METAL IONS.
CC -1- INDUCTION: BOTH MT-I AND MT-II GENES ARE REGULATED BY COPPER ION
CC IN A CONCENTRATION-DEPENDENT FASHION, AND BOTH ARE INDUCIBLE BY
CC SILVER BUT NOT BY CADMIUM SALTS.
CC -1- MISCELLANEOUS: MT-I MIGHT BIND APPROXIMATELY 11-12 MOL EQ OF
CC CU(II).
CC -1- SIMILARITY: BELONGS TO FAMILY 9 IN METALLOTHIONEIN SUPERFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; J05133; AAA35272.1; -.
CC DR PIR; A31252; A31252.
CC DR PIR; A34484; A34484.
CC DR HSSP; P04355; 4MT2.
CC KM Metal-binding; Metal-thiolate cluster; Chelation; Copper; Repeat.
CC FT INIT_MET 0
CC FT REPEAT 22 29
CC FT REPEAT 55 62
CC SQ SEQUENCE 62 AA; 6243 MW; 80D768C06C44F7A1 CRC64;

```

```

Query Match 100.0%; Score 53; DB 1; Length 62;
Best Local Similarity 19.0%; Pred. No. 56;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 CXXXCXXXXXXXXXXCXXC 21
DB 6 CPNCCSPNCANGCCGCCDC 26

```

```

OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Plekoyota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R.
RX MEDLINE=92102953; Pubmed=1684716;
RA Kuhn R., Kuhn C., Boersch D., Glaetzer K.H., Schaefer U.,
RA Schaefer M.;
RT "A cluster of four genes selectively expressed in the male germ line
RT of Drosophila melanogaster.";
RL Mech. Dev. 35:143-151(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY.
RX MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Planck C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher I., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ideyang C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -1- TISSUE SPECIFICITY: TESTIS.
CC -1- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCTES.
CC -1- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPETITIVE C-G-P
CC MOTIFS.
CC -1- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X67703; CAA47937.1; -.
CC DR EMBL; AF003672; AAF54022.1; -.
CC DR HSSP; P01180; INPO.
CC FLYBASE: Fbgn0004172; Mst84Da.

```

KW Spermatogenesis; Repeat: Multigene family.
SQ SEQUENCE 63 AA; 5806 MW; BF84CD7ACBCEFD3F CRC64;

Query Match 100.0%; Score 53; DB 1; Length 63;
Best Local Similarity 19.0%; Pred. No. 57;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXC 21
|::|::|::|::|::|::|
Db 16 CCGPCGCGPCGCGCGCGC 36

Search completed: March 1, 2001, 16:26:04
Job time: 401 sec